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*Animal Production Science*

### **Supplementary Material**

#### **Skim-Nanopore sequencing for routine genomic evaluation and bacterial pathogen detection in cattle**

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**Supplemental Table S1: Pathogens tested for using the quantitative real-time PCR**

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<b>Pathogen Name</b>
Bovine Herpes virus (DNA)
<i>Mycosplasma bovis</i>
<i>Histophilus Somni</i>
<i>Pasteurella multocida</i>
<i>Manheimia haemolytica</i>

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**Supplemental Table S2: Bovine respiratory disease pathogens of interest**

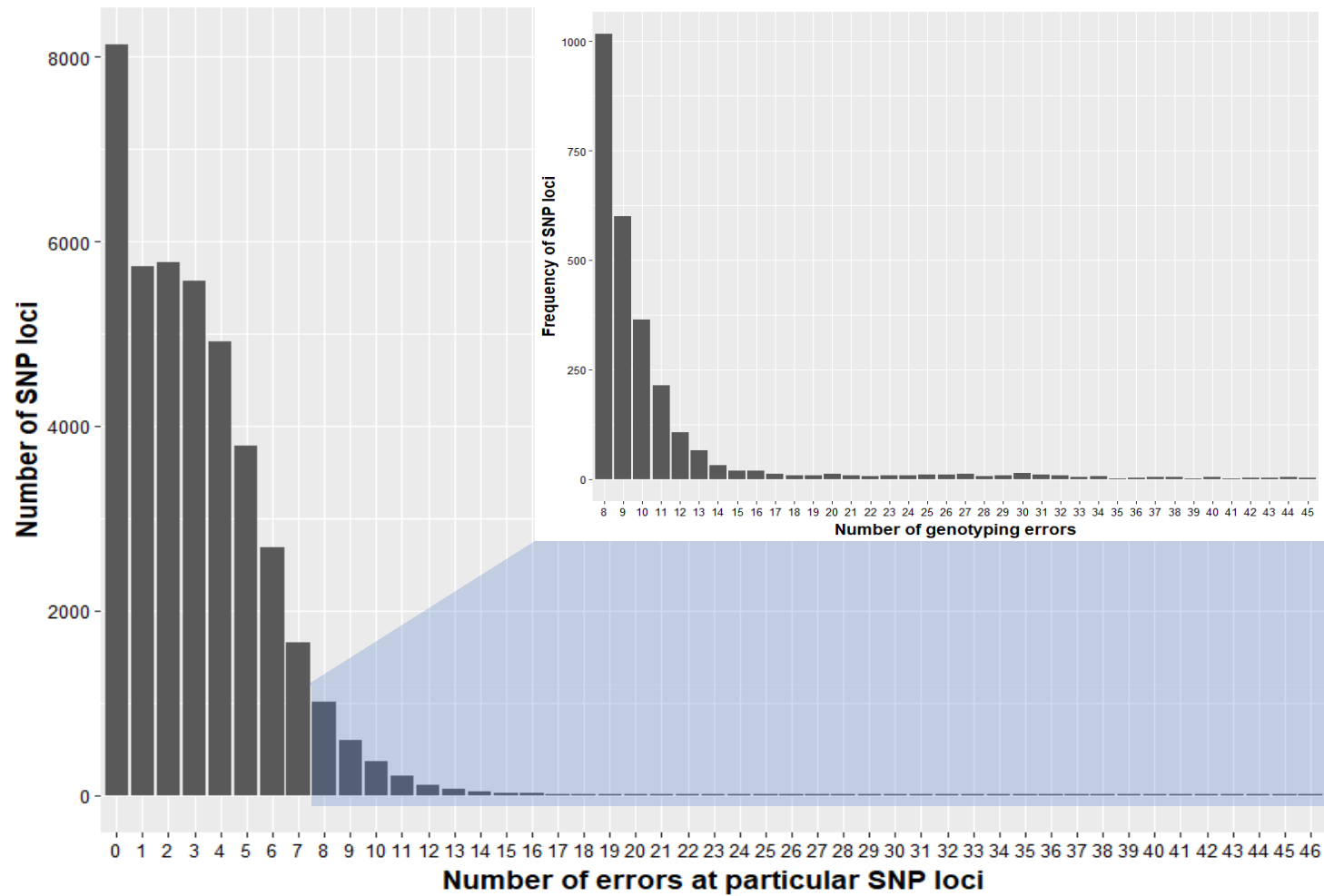
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<b>BRD associated pathogens</b>
Bovine Herpes virus (DNA)
<i>Mycosplasma spp.</i>
<i>Histophilus somni</i>
<i>Pasteurella multocida</i>
<i>Bibersteinia trehalosi</i>
<i>Mannheimia spp.</i>
<i>Moraxella spp.</i>
Ungulate parvo virus

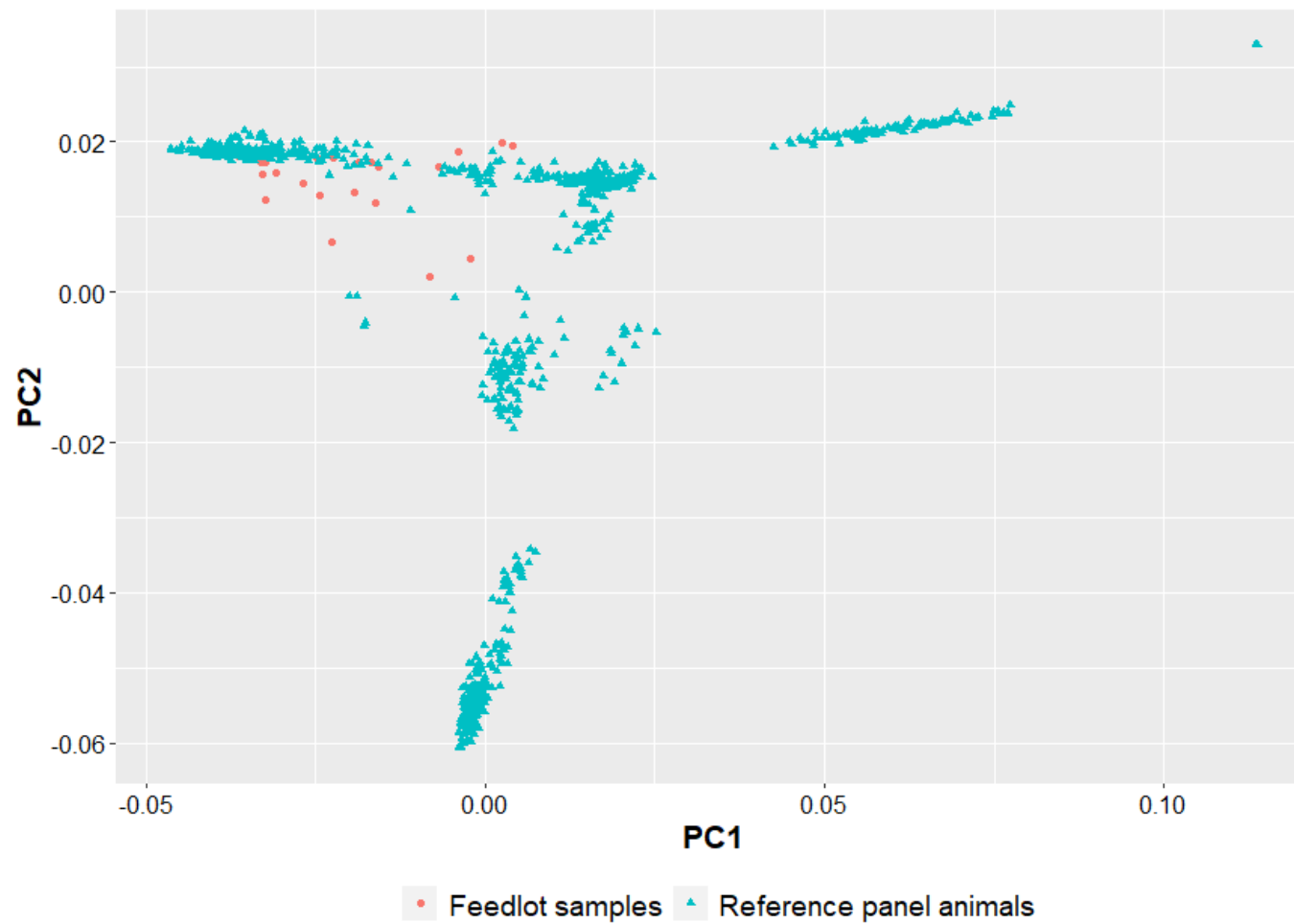
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**Supplemental Table S3: The amplification primer and dual labelled hydrolysis probe sequences used in the quantitative real-time PCR assays used to detect bovine respiratory disease associated pathogens this study.**

Target Species	Primer/Probe Designation	Primer/Probe Sequence (5' – 3')
Bovine alphaherpesvir us 1	BHVfwd	ATGTTAGCGCTCTGGAACC
	BHVrev	CTTTACGGTCGACGACTCC
	BHVprobe	Cy5-ACGGACGTGCGCGAAAAGA-BHQ2
<i>Mannheimia haemolytica</i>	Mhfwd	AAGGCGATGATATTCTCGATGGT
	Mhrev	TACCATCGCCTTTACGGTGAA
	Mhprobe	VIC-TATCGATGGCGGTAAAGGCAACGACCTA-BHQ1
<i>Pasteurella multocida</i>	Pmfwd	CGCAGGCAATGAATTCTCTTC
	Pmrev	GGCGCTCTTCAGCTGTTTTT
	PmProbe	Cy5-ACTGCACCAACAAATGCTTGCTGAGTTAGC-BHQ2
<i>Histophilus somni</i>	Hsfwd	AGGAAGGCGATTAGTTTAAGAGATTAATT
	Hsrev	TCACACCTCACTTAAGTCACCACCT
	Hsprobe	ROX-ATTGACGATAATCACAGAAGAAGCACCGGC-BHQ2
Mycoplasma bovis	MycoFWD	TGGGATAGCGGATGGAAACA
	MycoREV	GCTTCCTTTTATATTACTTTTCATGCAAC
	mycoProbe(MGB)	FAM-CCGATAATACCGAATACT-BHQ1



Supplemental Figure S1: Frequency distribution of the number of loci in the 40,878 overlapping SNP loci with 1 or more errors at that locus in the 48 samples. The inset shows the distribution of the systematic errors, i.e., having 8 or more errors at the loci out of the 48 animals.



**Supplemental Figure S2: Principal component analysis plot of the 48 sequenced feedlot samples and 1,205 animals in the reference panel used for genotyping and imputation.**